

Document made available under the Patent Cooperation Treaty (PCT)

International application number: PCT/US04/042358

International filing date: 17 December 2004 (17.12.2004)

Document type: Certified copy of priority document

Document details: Country/Office: US
Number: 60/530,547
Filing date: 17 December 2003 (17.12.2003)

Date of receipt at the International Bureau: 13 June 2005 (13.06.2005)

Remark: Priority document submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b)



World Intellectual Property Organization (WIPO) - Geneva, Switzerland
Organisation Mondiale de la Propriété Intellectuelle (OMPI) - Genève, Suisse

1330569

THE UNITED STATES OF AMERICA

TO ALL TO WHOM THESE PRESENTS SHALL COME:

UNITED STATES DEPARTMENT OF COMMERCE

United States Patent and Trademark Office

June 07, 2005

THIS IS TO CERTIFY THAT ANNEXED HERETO IS A TRUE COPY FROM THE RECORDS OF THE UNITED STATES PATENT AND TRADEMARK OFFICE OF THOSE PAPERS OF THE BELOW IDENTIFIED PATENT APPLICATION THAT MET THE REQUIREMENTS TO BE GRANTED A FILING DATE.

APPLICATION NUMBER: 60/530,547

FILING DATE: *December 17, 2003*

RELATED PCT APPLICATION NUMBER: *PCT/US04/42358*



Certified by

Under Secretary of Commerce
for Intellectual Property
and Director of the United States
Patent and Trademark Office



121703

16152 U.S. PTO

PTO/SB/16 (08-03)

Approved for use through 07/31/2006. OMB 0651-0032

U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

PROVISIONAL APPLICATION FOR PATENT COVER SHEET

This is a request for filing a PROVISIONAL APPLICATION FOR PATENT under 37 CFR 1.53(c).

Express Mail Label No. EL919126855US

22154 U.S. PTO
60/530547

121703

INVENTOR(S)					
Given Name (first and middle [if any])		Family Name or Surname		Residence (City and either State or Foreign Country)	
Liyan Wayne D.		He Frasch		Chandler, Arizona Phoenix, Arizona	
Additional inventors are being named on the _____ 0 _____ separately numbered sheets attached hereto					
TITLE OF THE INVENTION (500 characters max)					
Single Molecule Detection Using Molecular Motors					
Direct all correspondence to: CORRESPONDENCE ADDRESS					
<input checked="" type="checkbox"/> Customer Number:		28,529			
OR					
<input type="checkbox"/> Firm or Individual Name					
Address					
Address					
City		State		Zip	
Country		Telephone		Fax	
ENCLOSED APPLICATION PARTS (check all that apply)					
<input checked="" type="checkbox"/> Specification Number of Pages 13		<input type="checkbox"/> CD(s), Number _____			
<input checked="" type="checkbox"/> Drawing(s) Number of Sheets 2		<input checked="" type="checkbox"/> Other (specify) List accession nos. _____			
<input type="checkbox"/> Application Date Sheet. See 37 CFR 1.76					
METHOD OF PAYMENT OF FILING FEES FOR THIS PROVISIONAL APPLICATION FOR PATENT					
<input checked="" type="checkbox"/> Applicant claims small entity status. See 37 CFR 1.27.				FILING FEE Amount (\$) <div style="border: 1px solid black; width: 100px; height: 50px; margin: 0 auto; text-align: center;">80.00</div>	
<input checked="" type="checkbox"/> A check or money order is enclosed to cover the filing fees.					
<input checked="" type="checkbox"/> The Director is hereby authorized to charge filing fees or credit any overpayment to Deposit Account Number: 070135					
<input type="checkbox"/> Payment by credit card. Form PTO-2038 is attached.					
The invention was made by an agency of the United States Government or under a contract with an agency of the United States Government.					
<input type="checkbox"/> No.					
<input checked="" type="checkbox"/> Yes, the name of the U.S. Government agency and the Government contract number are: DARPA # N66001-03-C-XXXX.					

[Page 1 of 2]

Respectfully submitted,

SIGNATURE

TYPED or PRINTED NAME Thomas D. MacBlain

TELEPHONE 602-530-8088

Date

REGISTRATION NO. 24,583

(if appropriate)

Docket Number: 9138-0134

USE ONLY FOR FILING A PROVISIONAL APPLICATION FOR PATENT

This collection of information is required by 37 CFR 1.51. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 8 hours to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Mail Stop Provisional Application, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

FEE TRANSMITTAL for FY 2004

Effective 10/01/2003. Patent fees are subject to annual revision.

☒ Applicant claims small entity status. See 37 CFR 1.27

TOTAL AMOUNT OF PAYMENT (\$ 80.00

Complete if Known

Application Number
Filing Date herewith
First Named Inventor He
Examiner Name
Art Unit
Attorney Docket No. 9138-0134

METHOD OF PAYMENT (check all that apply)

☒ Check ☐ Credit card ☐ Money Order ☐ Other ☐ None

☒ Deposit Account:

Deposit Account Number 070135
Deposit Account Name Gallagher & Kennedy, P.A.

The Director is authorized to: (check all that apply)

☐ Charge fee(s) indicated below ☒ Credit any overpayments

☒ Charge any additional fee(s) or any underpayment of fee(s)

☐ Charge fee(s) indicated below, except for the filing fee to the above-identified deposit account.

FEE CALCULATION

1. BASIC FILING FEE

Large Entity	Small Entity	Fee Description	Fee Paid
Fee Code (\$)	Fee Code (\$)		
1001 770	2001 385	Utility filing fee	
1002 340	2002 170	Design filing fee	
1003 530	2003 265	Plant filing fee	
1004 770	2004 385	Reissue filing fee	
1005 160	2005 80	Provisional filing fee	80

SUBTOTAL (1) (\$ 80

2. EXTRA CLAIM FEES FOR UTILITY AND REISSUE

Total Claims	Extra Claims	Fee from below	Fee Paid
Independent Claims	-20** =	X	=
Multiple Dependent	-3** =	X	=

Large Entity	Small Entity	Fee Description
Fee Code (\$)	Fee Code (\$)	
1202 18	2202 9	Claims in excess of 20
1201 86	2201 43	Independent claims in excess of 3
1203 290	2203 145	Multiple dependent claim, if not paid
1204 86	2204 43	** Reissue independent claims over original patent
1205 18	2205 9	** Reissue claims in excess of 20 and over original patent

SUBTOTAL (2) (\$

**or number previously paid, if greater; For Reissues, see above

FEE CALCULATION (continued)

3. ADDITIONAL FEES

Large Entity Small Entity

Fee Code (\$)	Fee Code (\$)	Fee Description	Fee Paid
1051 130	2051 65	Surcharge - late filing fee or oath	
1052 50	2052 25	Surcharge - late provisional filing fee or cover sheet	
1053 130	1053 130	Non-English specification	
1812 2,520	1812 2,520	For filing a request for ex parte reexamination	
1804 920*	1804 920*	Requesting publication of SIR prior to Examiner action	
1805 1,840*	1805 1,840*	Requesting publication of SIR after Examiner action	
1251 110	2251 55	Extension for reply within first month	
1252 420	2252 210	Extension for reply within second month	
1253 950	2253 475	Extension for reply within third month	
1254 1,480	2254 740	Extension for reply within fourth month	
1255 2,010	2255 1,005	Extension for reply within fifth month	
1401 330	2401 165	Notice of Appeal	
1402 330	2402 165	Filing a brief in support of an appeal	
1403 290	2403 145	Request for oral hearing	
1451 1,510	1451 1,510	Petition to institute a public use proceeding	
1452 110	2452 55	Petition to revive - unavoidable	
1453 1,330	2453 665	Petition to revive - unintentional	
1501 1,330	2501 665	Utility issue fee (or reissue)	
1502 480	2502 240	Design issue fee	
1503 640	2503 320	Plant issue fee	
1460 130	1460 130	Petitions to the Commissioner	
1807 50	1807 50	Processing fee under 37 CFR 1.17(q)	
1806 180	1806 180	Submission of Information Disclosure Stmt	
8021 40	8021 40	Recording each patent assignment per property (times number of properties)	
1809 770	2809 385	Filing a submission after final rejection (37 CFR 1.129(a))	
1810 770	2810 385	For each additional invention to be examined (37 CFR 1.129(b))	
1801 770	2801 385	Request for Continued Examination (RCE)	
1802 900	1802 900	Request for expedited examination of a design application	

Other fee (specify)

*Reduced by Basic Filing Fee Paid

SUBTOTAL (3) (\$

SUBMITTED BY

(Complete (if applicable))

Name (Print/Type) Thomas D. MacBlain Registration No. 24,583 Telephone 602-530-8088
Signature [Signature] (Attorney/Agent) Date 6/17/03

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

This collection of information is required by 37 CFR 1.17 and 1.27. The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.14. This collection is estimated to take 12 minutes to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS.
SEND TO: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: He et al.
Filed: Herewith
Title: **SINGLE MOLECULE DETECTION USING MOLECULAR MOTORS**

CERTIFICATE OF MAILING BY EXPRESS MAIL
"Express Mail" mailing label number EL919126855US

Mail Stop Provisional Patent Application
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Commissioner:

I hereby certify that the following correspondence is being deposited in the United States Postal Service as Express Mail on the date shown below in an envelope addressed as shown above.

1. Provisional Application for Patent Cover Sheet (1 page);
2. Fee Transmittal for FY 2004 (1 page in duplicate);
3. Specification (13 pages plus cover sheet);
4. Figures (2 pages);
5. List of accession numbers for relevant F₁-ATPase sequences (29 pages);
6. Check for \$80.00; and
7. A return receipt postcard.

December 17, 2003
Date

Suzanne Shields
Suzanne Shields

GALLAGHER & KENNEDY, P.A.
2575 East Camelback Road
Phoenix, Arizona 85016-9255
Tel. No. (602) 530-8000
Fax. No. (602) 530-8500

Express Mail Label No. EL919126855US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Provisional Patent Application

**Title: SINGLE MOLECULE DETECTION USING MOLECULAR
MOTORS**

**Inventors: Liyan He, Chandler, Arizona
Wayne D. Frasch, Phoenix, Arizona**

**Attorneys for Applicant: Thomas D. MacBlain
Gallagher & Kennedy, P.A.
2575 East Camelback Road
Phoenix, AZ 85016-9225**

SINGLE MOLECULE DETECTION USING MOLECULAR MOTORS

Financial assistance for this project was provided by the U.S. Government, DARPA # N66001-03-C-XXXX; thus the United States Government has certain rights to this invention.

5 Various DNA hybridization methods have been developed in attempts to detect single molecules of nucleic acid (Singh-Zochhi et al., 2003; Castro et al., 1995, 1997, 2000). These methods have shown great potential for ultra-sensitive detection of nucleic acid. However they inherited the intrinsic limitation of DNA hybridization assays such as nonspecific binding, hybridization kinetics, and the requirement for a purified sample. The present invention provides methods that overcome the above limitations, thereby yielding higher sensitivity and accuracy
10 than other methods.

The present invention provides novel devices and methods for using such devices to detect a target nucleic acid sequence in a sample. The methods disclosed herein detect a DNA target as the result of ligation with two target-specific nucleic acids, which are ligated in the presence of the nucleic acid target. The thus-ligated product is used to bridge a molecular motor
15 and a detection probe. The probe reveals the motion imparted by the molecular motor to the bridging ligated product that is indicative of the nucleic acid target. The motion imparted to the probe is observed by an appropriately chosen means of detection. The methods of the invention are capable of detecting single molecules of the target nucleic acid, and thus provide an extremely sensitive technique for target detection that is of wide applicability, including but not
20 limited to clinical diagnostics, forensic analysis, gene expression analysis, and DNA sequencing.

Thus, in one aspect, the present invention provides methods for detecting a target nucleic acid comprising:

- (a) providing first and second target-specific nucleic acids, wherein the first and second target-specific nucleic acids each comprise sequences complementary to the target
25 nucleic acid; wherein the first target specific nucleic acid is bound to a first affinity tag and the second target-specific nucleic acid is bound to a second affinity tag, wherein the first affinity tag is capable of binding to a molecular motor, and wherein the second affinity tag is capable of binding to a detection probe;
- (b) contacting the first and second target-specific nucleic acids to a sample under
30 conditions whereby the first and second target-specific nucleic acids will hybridize to the target

nucleic acid if the target nucleic acid is present in the sample, wherein upon hybridization to the target nucleic acid the first and second target-specific nucleic acids are directly adjacent to each other;

(c) ligating the first and second target-specific nucleic acids together;

5 (d) binding the molecular motor to the first affinity tag and the detection probe to the second affinity tag;

(e) inducing movement of the molecular motor; and

(f) detecting movement of the molecular motor through the detection probe, wherein the movement of the molecular serves to detect the target nucleic acid in the sample.

10 The target nucleic acid can be any nucleic acid that can serve as a bridge between a molecular motor and a detection probe to detect motor-induced motion and for which the means of formation of that bridge is specific to that target nucleic acid. Thus, the target nucleic acid can comprise DNA or RNA and can be single stranded or double stranded. In a preferred embodiment, the target nucleic acid is double stranded. In a more preferred embodiment, the
15 target nucleic acid is a double stranded DNA.

. The first and second target specific nucleic acids can be any pair of nucleic acid sequences that are both complementary to the same target nucleic acid., so long as the first and second target specific nucleic acids are capable of hybridizing to adjacent segments of a target sequence so that the 3' end of the first target-specific nucleic acid is directly adjacent to the 5'
20 end of the second target-specific nucleic acid. There is no other specific nucleic acid sequence requirement for the first and second target specific nucleic acids.)- The first and second target specific nucleic acids can independently comprise DNA or RNA and can be single stranded or double stranded. In a preferred embodiment, the first and second target specific nucleic acids are both double stranded. In a more preferred embodiment, the first and second target specific
25 nucleic acids are both double stranded DNA.

As used herein the term "directly adjacent" means juxtaposed 5' phosphate and 3' hydroxyl termini of two adjacent target-specific nucleic acids hybridized to the complementary target nucleic acid, which can be ligated together by the action of a nucleic acid ligase.

The first affinity tag and the second affinity tag may be the same or different as is most
30 suitable for their ultimate attachment to the specific molecular motor and the detection probe employed. Preferably, the first and second affinity tags are different.

The first affinity tag can bind to the molecular motor and the second affinity tag can bind to the detection probe either directly (for example by a covalent bond between the target-specific nucleic acid and the affinity tag) or indirectly through another molecule. In a preferred embodiment, the first and second affinity tags bind indirectly to the molecular motor and the detection probe, respectively. In this preferred embodiment, the affinity tag binds directly to the target-specific nucleic acid sequence and to an affinity target, wherein the affinity target is bound to the molecular motor or the detection probe. Together, an affinity tag and affinity target make up a binding pair. Either member of a binding pair can be used as an affinity tag and either member can be used as an affinity target. An affinity target includes both separate molecules and portions of molecules, such as an epitope of a protein that interacts specifically with an affinity tag. Antibodies, either member of a receptor/ligand pair, and other molecules with specific binding affinities can be used as affinity tags. Binding an affinity tag to the target-specific nucleic acids thus permits an indirect linkage between the target-specific nucleic acids and the molecular motor or the detection probe. An affinity tag that interacts specifically with a particular affinity target is said to be specific for that affinity target. For example, an affinity tag which is an antibody that binds to a particular antigen is said to be specific for that antigen. Complementary nucleotide sequences can be used as binding pairs.

A non-limiting example of a binding pair is biotin/avidin. Other non-limiting binding pair examples include digoxigenin (DIG)/ anti-digoxigenin antibody and other antigen/antibody pairs. Epitope tags, such as a his-tag, and antibodies directed against the epitope tag (or fragments thereof) are further examples of binding pairs for use with the methods of the present invention. Those of skill in the art will understand that certain embodiments listed herein as indirect binding of the affinity tag and the molecular motor or detection probe can also be used for direct binding embodiments. For example, where the second affinity tag is an epitope tag as described above, the detection probe can be a labeled antibody against the epitope tag. Many further such examples will be readily apparent to those of skill in the art.

The affinity tags are bound to the first and second target-specific nucleic acids so as to not interfere with the ability of the first and second target-specific nucleic acids to be ligated together after hybridization to the target nucleic acid. In a preferred embodiment, one of the affinity tags is bound at or near the 5' end of one of the target specific nucleic acid sequences, and the other affinity tag is bound at or near the 3' end of the other target-specific nucleic acid

sequence, so as to permit juxtaposition of the 5' phosphate and 3' hydroxyl termini of the two adjacent target-specific nucleic acids at the desired site of ligation after hybridization of the target-specific nucleic acids to the target nucleic acid. Such design of the target-specific nucleic acids and the affinity tags is well within the level of skill of those in the art.

5 The sample in which detection of the target nucleic acid is to be assessed can be any sample of interest, including but not limited to genomic DNA, cell lysates, tissue homogenates, forensic samples, environmental samples, and isolated nucleic acid samples from cells, tissues, or complete organisms.

10 Optimization of conditions for contacting the first and second target-specific nucleic acids to a sample under conditions whereby the first and second target-specific nucleic acids will hybridize to the target nucleic acid if the target nucleic acid is present in the sample can be readily accomplished by those of skill in the art. The hybridization conditions are thus optimized to limit hybridization/ligation to those situations where the target nucleic acid is present. Such optimization includes consideration of the nucleic acid probe sequence and length, reaction
15 buffer, reaction temperature, and reaction time.

The ligation step of the methods of the invention can be accomplished by techniques known to those of skill in the art using commercially available nucleic acid ligases. Any DNA ligase is suitable for use in the disclosed method. Preferred ligases are those that preferentially form phosphodiester bonds at nicks in double-stranded DNA. That is, ligases that fail to ligate
20 the free ends of single-stranded DNA at a significant rate are preferred. Thermostable ligases are especially preferred. Many suitable ligases are known, such as T4 DNA ligase (Davis et al., Advanced Bacterial Genetics--A Manual for Genetic Engineering (Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1980)), E. coli DNA ligase (Panasnko et al., J Biol. Chem. 253:4590-4592 (1978)), AMPLIGASE.RTM. (Kalin et al., Mutat Res., 283(2):119-123
25 (1992); Winn-Deen et al., Mol Cell Probes (England) 7(3):179-186 (1993)), Taq DNA ligase (Barany, Proc. Natl. Acad Sci. USA 88:189-193 (1991)), Thermus thermophilus DNA ligase (Abbott Laboratories), Thermus scotoductus DNA ligase and Rhodothermus marinus DNA ligase (Thorbjarnardottir et al., Gene 151:177-180 (1995)). T4 DNA ligase is preferred for ligations involving RNA target sequences due to its ability to ligate DNA ends involved in
30 DNA:RNA hybrids (Hsuih et al., Quantitative detection of HCV RNA using novel ligation-

dependent polymerase chain reaction, American Association for the Study of Liver Diseases (Chicago, IL, Nov. 3-7, 1995)).

In a most preferred embodiment, ligation is accomplished by use of a ligation chain reaction. The term "ligation chain reaction" ("LCR") describes the process pioneered by Landegren et al. (1988 Science 241, 1077-1080). This process detects the presence of given DNA sequences based on the ability of two probes to anneal directly adjacent to each other on a complementary target DNA molecule. The two probes are then joined covalently by the action of a DNA ligase, provided that the nucleotides at the junction are correctly base-paired. Thus single nucleotide substitutions can be distinguished. This strategy permits the rapid and standardized identification of single-copy gene sequences in genomic DNA. Furthermore, due to its high specificity, LCR can be performed in crude samples, without the need for purifying the nucleic acid target, which significantly simplifies the assay process.

The disclosed method detects target nucleic acid through ligation chain reaction (Cheng et al., 1996) to generate a DNA sequence that has affinity tags on both ends so that it can serve as a bridge between the molecular motor and the detection probe. Ligation chain reaction requires the formation of juxtaposed 5' phosphate and 3' hydroxyl termini of the two adjacent target-specific nucleic acids, which are hybridized to a complementary nucleic acid target. The ligation will occur only if the target-specific nucleic acids are perfectly paired to the target nucleic acid and have no gap between them. Therefore, this method is much more specific than hybridization alone and a single-base substitution can be easily detected. In the disclosed methods using double stranded target-specific nucleic acids and target nucleic acid, thousands of copies of the ligated products can be generated from a single copy of target nucleic acid. LCR does not actually copy the target itself. However, after the first pair of target-specific nucleic acids is ligated, double stranded DNA products can be denatured at higher temperature to allow another pair of target-specific nucleic acid probes to hybridize to the same target, followed by further ligation. The process is similar to PCR except the target molecules are not being copied. In this embodiment, thermal cycling is most preferred. In a non-limiting example, conditions employed include an initial hybridization step at 95°C for two minutes, followed by 19 cycles of 1 minute at 95°C and 4 minutes at 65°C in the presence of a thermostable DNA ligase and appropriate reaction components. Those of skill in the art are well-versed in modifying such cycling

conditions to provide optimal hybridization based on the use of different nucleic acid sequences or different buffer conditions.

The molecular motors of the invention include any biological or synthetic molecule capable of induced translational or rotational movements that are capable of detection. In a preferred embodiment, the molecular motor is a biomolecular motor. Non-limiting examples of such biomolecular motors are F₁-ATPases (see, for example, the attached list of accession number for relevant F₁-ATPase sequences), actomyosin, ciliary axonemes, bacteria flagellar motors, kinesin/microtubules, and nucleic acid helicases and polymerases. In some cases the molecular motor may need to be immobilized (i.e. secured in place) for detection. For example, it may be necessary to immobilize the molecular motor if the rotation needs to be visualized or if the detection depends on the perturbation of the local environment such as micro current or impedance. A series of molecular motors can be immobilized on a surface to generate a molecular motor array. If each motor is coated with different affinity targets and different first target-specific nucleic acids (specific to the same or different target nucleic acids) are labeled with different affinity tags, this molecular motor array can be used to detect multiple target nucleic acids in such manner similar to a gene chip. As used herein, an "array" comprises a solid surface, with molecular motors attached to said surface. Arrays typically comprise a plurality of molecular motor linked to different capture groups that are coupled to a surface of a substrate in different, known locations. For example, there are several silane derivatives to attach a variety of functional groups to a glass surface. The term "solid surface" as used herein refers to a material having a rigid or semi-rigid surface. Such materials will preferably take the form of chips, plates, slides, cover slips, small beads, pellets, disks or other convenient forms, although other forms may be used. The surfaces are generally coated with an affinity target.

In a preferred embodiment, the first affinity tag attaches to a moiety on the moving component of the motor. By way of example, the rotating subunits on the F₁-ATPase include the γ and ϵ subunits, while the α , β , and δ subunits do not rotate. The γ subunit is currently strongly preferred because the ϵ subunit acts as an ATPase inhibitor. Thus, where the F₁-ATPase is used as the molecular motor, it is preferred that the first affinity tag bind (directly or indirectly) to the γ subunit, while the molecular motor is attached to a substrate through the α , β , or δ subunits. The α or β subunits are currently preferred because they provide a three-point attachment due to the stoichiometry of these subunits in the protein. For example, the

“moiety” may be a cysteine residue created by site-directed mutagenesis at a specific position of a protein-based biomolecular motor, such as the γ subunit of F1-ATPase. The first affinity tag can be attached to the cysteine residue through linkage to its sulfhydryl group. Alternatively, an affinity target can be used to coat the molecular motor, and can interact with the affinity tag.

5 This molecular motor coated with affinity targets can then be linked specifically to the affinity tag on the first target-specific nucleic acid. As will be apparent to one of skill in the art, site directed mutagenesis can be used to introduce a cysteine residue (or other useful residues) to various protein-based biomolecular motors so that they can be linked to affinity tags. Furthermore, there are a variety of covalent modification reagents that can modify specific amino
10 acid side chains.

The detection probe can be anything that is capable of attaching to the affinity tag on the second target-specific nucleic acid and providing a means of detecting the movement generated by the molecular motor, such as metallic nanoparticles (rods, spheres, quantum dots, etc.) fluorescent dyes, and nanoparticles labeled with fluorescent dyes. In a non-limiting example,
15 gold rod detection probes capable of visual observation by microscope are attached to the second target-specific nucleic acid through a biotin bond. In a non-limiting embodiment, the gold nanorod is coated with anti-DIG antibody (the affinity target), which binds specifically to a DIG (Digoxigenin) second affinity tag. In another preferred embodiment, the gold nanorods can directly link to alkanethio modified oligonucleotides.

20 Inducing movement of the molecular motor is done by standard methods in the art for a given molecular motor. For example, the movement of F1 ATPases is induced by adding ATP (Noji, H., Yasuda, R., Yoshida, M. and Kinosita, K. (1997) Nature 386, 299-302). Those of skill in the art are able to determine how to induce movement of other known molecular motors using similar published protocols. The only motion that will be detected will result from molecular
25 motors that are connected to the detection probe. Since that will depend upon the presence of the nucleic acid bridge resulting from specific hybridization of the target specific nucleic acids and the target nucleic acid (and the subsequent ligation), observation of this motion will identify the presence of the target nucleic acid.

Detecting movement of the molecular motor through the detection probe can be
30 accomplished by any suitable means. In one embodiment, direct visualization of the movement is used. In a non-limiting example, gold rod detection probes capable of visual observation by

microscope are attached to the second target-specific nucleic acid through a biotin/avidin interaction. Other means of observation include, but are not limited to single molecule fluorescence resonance energy transfer, fluorescence lifetime anisotropy, and atomic force microscopy. Beside microscopy, other methods can be used to observe the rotation of detection probe, including but not limited to: (1) attaching the molecular motor onto a nano-electrode and measure the micro current change or impedance change produced by rotation; (2) Measuring single molecule anisotropy; (3) Using a surface plasmon resonance biosensor to measure the surface plasmon resonance change during metallic nanorods rotation; and (4) Attaching a fluorescent label such as Pacific Blue (Molecular Probes) on non-rotating part of the molecular motor. Rotation can be observed through periodic quenching of the fluorescence signal by a quencher detection probe attached to the rotating part of the molecular motor. Alternatively, the fluorescent label can be attached to the rotating part of the molecular motor and the quencher can be linked to the non-rotating part. .

Since the methods of the invention are capable of detecting single molecules of a target, they provide a precise means to quantify the amount of target present. In one embodiment, the number of rotating molecules is determined by visualization and a calculation is made for the fraction of the total sample that is being viewed. This is not possible with fluorescent detection methods in current use with DNA microarrays.

Example 1

As shown in Fig. 1, one embodiment of the disclosed methods comprises the following steps:

1. As indicated in Fig. 1a, a first affinity tag is attached to the 5' end of the first target-specific DNA strand. A second affinity tag is attached to the 3' end of second target-specific DNA strand. The second target-specific DNA strand is phosphorylated either during chemical synthesis, or after synthesis using a polynucleotide kinase (Fig. 1a).

2. In Fig. 1b the first and second target-specific nucleic acid strands are hybridized to the target nucleic acid so that the 3' end of the first target-specific strand is directly adjacent to the 5' end of the second target-specific strand.

3. In Fig. 1c the first and second target-specific DNA strands are ligated, to generate a double-stranded DNA sequence in which one of the strands contains the first and the second affinity tags at the 5' and 3' ends, respectively.

4. In Fig. 1d the double-stranded DNA that contains the affinity tags is then used as a bridge between a molecular motor and the detection probe used to detect the motion generated from the motor via the affinity tags. The first affinity tag attaches specifically to a moiety on a moving component of the molecular motor while the second affinity tag is specific to the detection probe. In the specific preferred and exemplary embodiment the first affinity tag, a biotin, binds to an avidin attached to the rotating part of the motor and therefore links the motor to the first target-specific nucleic acid. The motor shown is the F₁-ATPase biomolecular motor. In the specific example, the detection probe comprises gold nanorods that can be visualized by microscopy, attached to the second target-specific nucleic acid through interactions between digoxigenin (DIG) and anti-digoxigenin antibody. The particular gold rods are of such sizes that they efficiently scatter red and green light from their long and short axes, respectively, such that when viewed through a polarizing filter with dark-field microscopy, the rotating rods appear as alternating red and green spots.

5. Immobilization occurs after assembly of the components in step 4 (Fig. 2a). Immobilization is effected by histadine binding of the nonrotational F₁ motor structure to a nickel surface.

6. The movement of the molecular motor is induced by adding ATP (Fig. 2b). The only motion that is detected results from motors that are connected to the attached detection probe. Since that depends upon the presence of the double-stranded DNA bridge and because the double stranded DNA only results from the specific hybridization to the target DNA, observation of this motion identifies the presence of the target DNA.

Example 2

The following are two examples for detecting multiple target nucleic acids simultaneously:

Approach 1: Detection probes comprising gold rods of different sizes are used to detect ligated DNAs that are specific to pBR322 and Lambda DNA simultaneously using the following procedures:

1. Gold nanorods of different lengths are prepared because the length determines the wavelength of light scattered from it. The short and long gold rods are prepared to enable them to bind to digoxigenin (DIG) and dinitrophenyl-X (DNP-X), respectively.
2. Two pair of target-specific nucleic acids are prepared that are designed to hybridize specifically with pBR322 and Lambda DNA, respectively.
3. To enable the target-specific nucleic acid pairs to bridge between F₁ ATPase and a gold nanorod, one target-specific nucleic acid from each pair is labeled with biotin while the other target-specific nucleic acid is labeled with DIG and DNP-X for pBR322 and Lambda DNA, respectively.
4. LCR is performed with the two target-specific nucleic acid pairs.
5. The ligated products are linked to avidin-coated F₁ ATPase through biotin/avidin binding.
6. The assembly is completed upon attachment of the gold nanorods of different lengths.
7. Observation of ATP-dependent rotation of different colored nanorods indicates the presence of the corresponding target.

Approach 2: Ligated DNAs that are specific to pBR322 and Lambda DNA are detected simultaneously on an antibody-coated-F₁ ATPase array using the following procedures:

1. F₁-ATPase is prepared to enable binding to either anti-DIG antibody and anti-DNP antibody, respectively.
2. Anti-DIG-coated F₁ ATPase and anti-DNP-coated F₁ ATPase are immobilized on different locations on a cover slip.
3. Two pairs of target-specific nucleic acids are prepared that are designed to hybridize specifically with pBR322 and Lambda DNA, respectively.
4. To enable the target-specific nucleic acid pairs to bridge between F₁ ATPase and a gold nanorod, one target-specific nucleic acid of each pair is labeled with biotin while the other target-specific nucleic acid is labeled with DIG and DNP-X for pBR322 and Lambda DNA, respectively.
5. LCR is performed with the two target-specific nucleic acid pairs.

6. The ligated products from pBR322 and Lambda DNA are linked to anti-DIG-coated F₁ ATPase anti-DNP-coated F₁ ATPase, respectively.

7. The assembly is completed upon attachment of the avidin coated gold nanorods.

8. Observation of ATP-dependent rotation at different location on the cover slip indicates
5 the presence of the corresponding target nucleic acid.

In another aspect, the present invention provides kits for nucleic acid detection comprising first and second target-specific nucleic acids, wherein the first and second target-specific nucleic acids each comprise sequences complementary to a target nucleic acid, wherein upon hybridization to the target nucleic acid the first and second target-specific nucleic acids will
10 be directly adjacent to each other; wherein the first target specific nucleic acid is bound to a first affinity tag and the second target-specific nucleic acid is bound to a second affinity tag, wherein the first affinity tag is capable of binding to a molecular motor, and wherein the second affinity tag is capable of binding to a detection probe.

In preferred embodiments, the kit further contains a molecular motor that binds to the
15 first affinity tag and/or a detection probe that binds to the second affinity tag. In a further embodiment, the molecular motor is bound to a solid support, such as a glass coverslip or other suitable support. The support can be derivatized in any manner suitable for binding to the molecular motor.

The present invention also provides a composition comprising first and second target-specific nucleic acids base-paired with a target nucleic acid and directly adjacent to each other,
20 wherein the first target specific nucleic acid is bound to a first affinity tag capable of binding to a molecular motor and the second target-specific nucleic acid is bound to a second affinity tag capable of binding to a detection probe. In a further embodiment, the first and second target-specific nucleic acid sequences are ligated together.

25 The present invention also provides a composition comprising:

(a) a nucleic acid complex comprising a first target-specific nucleic acid bound to a first affinity tag capable of binding to a molecular motor; a second target-specific nucleic acid bound to a second affinity tag capable of binding to a detection probe, and a target nucleic acid, wherein the first and second target-specific nucleic acids are base-paired with the target nucleic
30 acid and ligated together;

(b) a molecular motor bound to the first affinity tag; and

(c) a detection probe bound to the second affinity tag.

The present invention further provides a composition comprising:

(a) a solid support; and

(b) a plurality of molecular motors attached to the solid support, wherein the plurality

5 of molecular motors comprise an affinity target for binding to a specific affinity tag.

In a preferred embodiment, the plurality of molecular motors comprises more than one type of molecular motor. In a further preferred embodiment, the different types of molecular motors on the support comprise different affinity targets that are specific for different affinity tags. In a further preferred embodiment, the composition further comprises a first target-specific
10 nucleic acid bound to a first affinity tag that binds to the affinity target on the molecular motor. In a further preferred embodiment, the first target specific nucleic acid is hybridized to a target nucleic acid, and the target nucleic acid is further hybridized to a second target-specific nucleic acid that is bound to a second affinity tag, wherein the second affinity tag is bound to a detection probe.

References

1. Castro, A., T. R. Okinaka, "Ultrasensitive, Direct Detection of a Specific DNA Sequence of *Bacillus anthracis* in Solution," *The Analyst* 125, 9-11 (2000).
2. Castro, A., Williams, J., "Single-Molecule Detection of Specific Nucleic Acid Sequences in Unamplified Genomic DNA," *Analytical Chemistry* 69, 3915-3920 (1997).
3. Castro, A., Shera, E. B., "Single-Molecule Electrophoresis," *Analytical Chemistry* 67, 3181-3186 (1995).
4. Cheng, J., Shoffner, M. A., Mitchelson, K. R., Kricka, L. J., Wilding, P. (1996) Analysis of ligase chain reaction (LCR) products amplified in a silicon chip using entangled solution capillary electrophoresis (ESCE), *J. Chromatogr A* 732:151-8.
5. Singh-Zocchi, Mukta, Dixit, Sanhita, Ivanor, Vassili, Zocchi, Giovanni (2003) *PNAS* 100:7605-7610.
6. A manual for genetic engineering. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1980
7. Panasenko et al., (1978) *J Biol. Chem.* 253:4590-4592.
8. Kalin et al., (1992) *Mutat Res.*, 283(2):119-123.
9. Winn-Deen et al., (1993) *Mol Cell Probes (England)* 7(3):179-186).
10. Barany, (1991) *Proc. Natl. Acad Sci. USA* 88:189-193
11. Thorbjarnardottir et al., (1995) *Gene* 151:177-180).
12. Hsuih et al., (1995) Quantitative detection of HCV RNA using novel ligation-dependent polymerase chain reaction, *American Association for the Study of Liver Diseases (Chicago, IL, Nov. 3-7.*
12. Landegren et al., (1988) *Science* 241, 1077-1080.

Figure 1

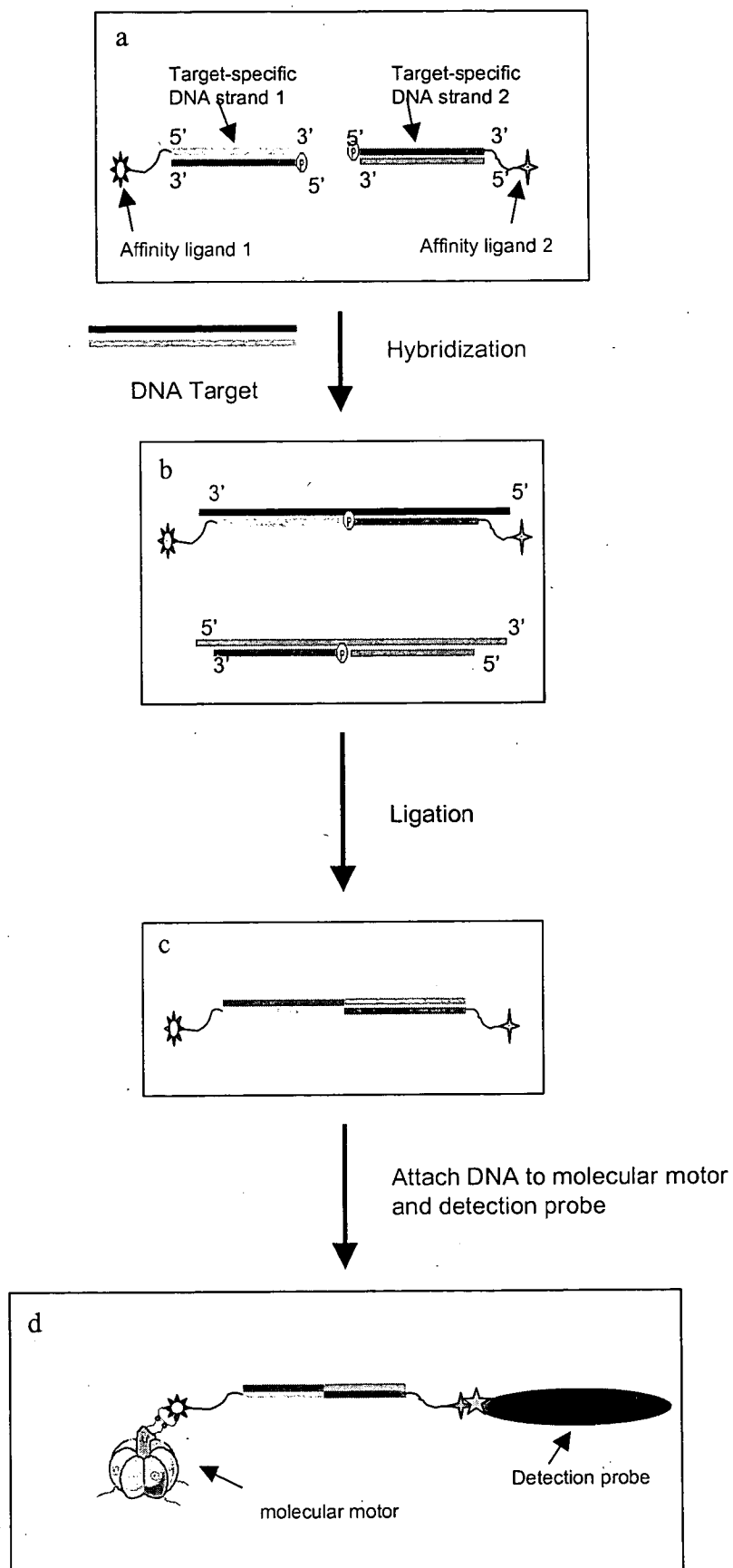


Figure 2

